

## SEQUENCE LISTING

<110> HEGEMANN, Peter

<120> USE OF BIOLOGICAL PHOTORECEPTORS AS DIRECTLY LIGHT-CONTROLLED  
ION CHANNELS

<130> 231181

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 712

<212> PRT

<213> Chlamydomonas reinhardtii

<220>

<223> Amino acid sequence of CHOP-1 (AF461397) from  
Chlamydomonas reinhardtii

<400> 1

Met Ser Arg Arg Pro Trp Leu Leu Ala Leu Ala Leu Ala Val Ala Leu  
1 5 10 15

Ala Ala Gly Ser Ala Gly Ala Ser Thr Gly Ser Asp Ala Thr Val Pro  
20 25 30

Val Ala Thr Gln Asp Gly Pro Asp Tyr Val Phe His Arg Ala His Glu  
35 40 45

Arg Met Leu Phe Gln Thr Ser Tyr Thr Leu Glu Asn Asn Gly Ser Val  
50 55 60

Ile Cys Ile Pro Asn Asn Gly Gln Cys Phe Cys Leu Ala Trp Leu Lys  
65 70 75 80

Ser Asn Gly Thr Asn Ala Glu Lys Leu Ala Asn Ile Leu Gln Trp  
85 90 95

Ile Thr Phe Ala Leu Ser Ala Leu Cys Leu Met Phe Tyr Gly Tyr Gln  
100 105 110

Thr Trp Lys Ser Thr Cys Gly Trp Glu Glu Ile Tyr Val Ala Thr Ile  
115 120 125

Glu Met Ile Lys Phe Ile Ile Glu Tyr Phe His Glu Phe Asp Glu Pro  
130 135 140

Ala Val Ile Tyr Ser Ser Asn Gly Asn Lys Thr Val Trp Leu Arg Tyr  
145 150 155 160

Ala Glu Trp Leu Leu Thr Cys Pro Val Ile Leu Ile His Leu Ser Asn  
165 170 175

Leu Thr Gly Leu Ala Asn Asp Tyr Asn Lys Arg Thr Met Gly Leu Leu  
 180 185 190  
 Val Ser Asp Ile Gly Thr Ile Val Trp Gly Thr Thr Ala Ala Leu Ser  
 195 200 205  
 Lys Gly Tyr Val Arg Val Ile Phe Phe Leu Met Gly Leu Cys Tyr Gly  
 210 215 220  
 Ile Tyr Thr Phe Phe Asn Ala Ala Lys Val Tyr Ile Glu Ala Tyr His  
 225 230 235 240  
 Thr Val Pro Lys Gly Ile Cys Arg Asp Leu Val Arg Tyr Leu Ala Trp  
 245 250 255  
 Leu Tyr Phe Cys Ser Trp Ala Met Phe Pro Val Leu Phe Leu Leu Gly  
 260 265 270  
 Pro Glu Gly Phe Gly His Ile Asn Gln Phe Asn Ser Ala Ile Ala His  
 275 280 285  
 Ala Ile Leu Asp Leu Ala Ser Lys Asn Ala Trp Ser Met Met Gly His  
 290 295 300  
 Phe Leu Arg Val Lys Ile His Glu His Ile Leu Leu Tyr Gly Asp Ile  
 305 310 315 320  
 Arg Lys Lys Gln Lys Val Asn Val Ala Gly Gln Glu Met Glu Val Glu  
 325 330 335  
 Thr Met Val His Glu Glu Asp Asp Glu Thr Gln Lys Val Pro Thr Ala  
 340 345 350  
 Lys Tyr Ala Asn Arg Asp Ser Phe Ile Ile Met Arg Asp Arg Leu Lys  
 355 360 365  
 Glu Lys Gly Phe Glu Thr Arg Ala Ser Leu Asp Gly Asp Pro Asn Gly  
 370 375 380  
 Asp Ala Glu Ala Asn Ala Ala Ala Gly Gly Lys Pro Gly Met Glu Met  
 385 390 395 400  
 Gly Lys Met Thr Gly Met Gly Met Gly Ala Gly Met Gly Met  
 405 410 415  
 Ala Thr Ile Asp Ser Gly Arg Val Ile Leu Ala Val Pro Asp Ile Ser  
 420 425 430  
 Met Val Asp Phe Phe Arg Glu Gln Phe Ala Arg Leu Pro Val Pro Tyr  
 435 440 445  
 Glu Leu Val Pro Ala Leu Gly Ala Glu Asn Thr Leu Gln Leu Val Gln  
 450 455 460  
 Gln Ala Gln Ser Leu Gly Gly Cys Asp Phe Val Leu Met His Pro Glu

465	470	475	480
Phe Leu Arg Asp Arg Ser Pro Thr Gly		Leu Leu Pro Arg Leu Lys Met	
485		490	495
Gly Gly Gln Arg Ala Ala Ala Phe Gly	Trp Ala Ala Ile Gly Pro Met		
500	505		510
Arg Asp Leu Ile Glu Gly Ser Gly Val Asp Gly Trp Leu Glu Gly Pro			
515	520		525
Ser Phe Gly Ala Gly Ile Asn Gln Gln Ala Leu Val Ala Leu Ile Asn			
530	535		540
Arg Met Gln Gln Ala Lys Lys Met Gly Met Met Gly Gly Met Gly Met			
545	550	555	560
Gly Met Gly Gly Met Gly Met Gly Met Gly Met Gly Met Gly Met			
565	570		575
Ala Pro Ser Met Asn Ala Gly Met Thr Gly Gly Met Gly Gly Ala Ser			
580	585		590
Met Gly Gly Ala Val Met Gly Met Gly Met Gly Met Gln Pro Met Gln			
595	600		605
Gln Ala Met Pro Ala Met Ser Pro Met Met Thr Gln Gln Pro Ser Met			
610	615		620
Met Ser Gln Pro Ser Ala Met Ser Ala Gly Gly Ala Met Gln Ala Met			
625	630	635	640
Gly Gly Val Met Pro Ser Pro Ala Pro Gly Gly Arg Val Gly Thr Asn			
645	650		655
Pro Leu Phe Gly Ser Ala Pro Ser Pro Leu Ser Ser Gln Pro Gly Ile			
660	665		670
Ser Pro Gly Met Ala Thr Pro Pro Ala Ala Thr Ala Ala Pro Ala Ala			
675	680		685
Gly Gly Ser Glu Ala Glu Met Leu Gln Gln Leu Met Ser Glu Ile Asn			
690	695		700
Arg Leu Lys Asn Glu Leu Gly Glu			
705	710		
<210> 2			
<211> 737			
<212> PRT			
<213> Chlamydomonas reinhardtii			
<220>			
<223> Amino acid sequence of CHOP-2 (AF461397) from Chlamydomonas reinhardtii			

&lt;400&gt; 2

Met Asp Tyr Gly Gly Ala Leu Ser Ala Val Gly Arg Glu Leu Leu Phe  
 1 5 10 15

Val Thr Asn Pro Val Val Val Asn Gly Ser Val Leu Val Pro Glu Asp  
 20 25 30

Gln Cys Tyr Cys Ala Gly Trp Ile Glu Ser Arg Gly Thr Asn Gly Ala  
 35 40 45

Gln Thr Ala Ser Asn Val Leu Gln Trp Leu Ala Ala Gly Phe Ser Ile  
 50 55 60

Leu Leu Leu Met Phe Tyr Ala Tyr Gln Thr Trp Lys Ser Thr Cys Gly  
 65 70 75 80

Trp Glu Glu Ile Tyr Val Cys Ala Ile Glu Met Val Lys Val Ile Leu  
 85 90 95

Glu Phe Phe Phe Glu Phe Lys Asn Pro Ser Met Leu Tyr Leu Ala Thr  
 100 105 110

Gly His Arg Val Gln Trp Leu Arg Tyr Ala Glu Trp Leu Leu Thr Cys  
 115 120 125

Pro Val Ile Leu Ile His Leu Ser Asn Leu Thr Gly Leu Ser Asn Asp  
 130 135 140

Tyr Ser Arg Arg Thr Met Gly Leu Leu Val Ser Asp Ile Gly Thr Ile  
 145 150 155 160

Val Trp Gly Ala Thr Ser Ala Met Ala Thr Gly Tyr Val Lys Val Ile  
 165 170 175

Phe Phe Cys Leu Gly Leu Cys Tyr Gly Ala Asn Thr Phe Phe His Ala  
 180 185 190

Ala Lys Ala Tyr Ile Glu Gly Tyr His Thr Val Pro Lys Gly Arg Cys  
 195 200 205

Arg Gln Val Val Thr Gly Met Ala Trp Leu Phe Phe Val Ser Trp Gly  
 210 215 220

Met Phe Pro Ile Leu Phe Ile Leu Gly Pro Glu Gly Phe Gly Val Leu  
 225 230 235 240

Ser Val Tyr Gly Ser Thr Val Gly His Thr Ile Ile Asp Leu Met Ser  
 245 250 255

Lys Asn Cys Trp Gly Leu Leu Gly His Tyr Leu Arg Val Leu Ile His  
 260 265 270

Glu His Ile Leu Ile His Gly Asp Ile Arg Lys Thr Thr Lys Leu Asn  
 275 280 285

Ile Gly Gly Thr Glu Ile Glu Val Glu Thr Leu Val Glu Asp Glu Ala  
 290 295 300  
 Glu Ala Gly Ala Val Asn Lys Gly Thr Gly Lys Tyr Ala Ser Arg Glu  
 305 310 315 320  
 Ser Phe Leu Val Met Arg Asp Lys Met Lys Glu Lys Gly Ile Asp Val  
 325 330 335  
 Arg Ala Ser Leu Asp Asn Ser Lys Glu Val Glu Gln Glu Gln Ala Ala  
 340 345 350  
 Arg Ala Ala Met Met Met Asn Gly Asn Gly Met Gly Met Gly Met  
 355 360 365  
 Gly Met Asn Gly Met Asn Gly Met Gly Gly Met Asn Gly Met Ala Gly  
 370 375 380  
 Gly Ala Lys Pro Gly Leu Glu Leu Thr Pro Gln Leu Gln Pro Gly Arg  
 385 390 395 400  
 Val Ile Leu Ala Val Pro Asp Ile Ser Met Val Asp Phe Phe Arg Glu  
 405 410 415  
 Gln Phe Ala Gln Leu Ser Val Thr Tyr Glu Leu Val Pro Ala Leu Gly  
 420 425 430  
 Ala Asp Asn Thr Leu Ala Leu Val Thr Gln Ala Gln Asn Leu Gly Gly  
 435 440 445  
 Val Asp Phe Val Leu Ile His Pro Glu Phe Leu Arg Asp Arg Ser Ser  
 450 455 460  
 Thr Ser Ile Leu Ser Arg Leu Arg Gly Ala Gly Gln Arg Val Ala Ala  
 465 470 475 480  
 Phe Gly Trp Ala Gln Leu Gly Pro Met Arg Asp Leu Ile Glu Ser Ala  
 485 490 495  
 Asn Leu Asp Gly Trp Leu Glu Gly Pro Ser Phe Gly Gln Gly Ile Leu  
 500 505 510  
 Pro Ala His Ile Val Ala Leu Val Ala Lys Met Gln Gln Met Arg Lys  
 515 520 525  
 Met Gln Gln Met Gln Gln Ile Gly Met Met Thr Gly Gly Met Asn Gly  
 530 535 540  
 Met Gly Gly Gly Met Gly Gly Met Asn Gly Met Gly Gly Gly Asn  
 545 550 555 560  
 Gly Met Asn Asn Met Gly Asn Gly Met Gly Gly Met Gly Asn Gly  
 565 570 575  
 Met Gly Gly Asn Gly Met Asn Gly Met Gly Gly Gly Asn Gly Met Asn  
 580 585 590

Asn Met Gly Gly Asn Gly Met Ala Gly Asn Gly Met Gly Gly Met  
 595 600 605

Gly Gly Asn Gly Met Gly Gly Ser Met Asn Gly Met Ser Ser Gly Val  
 610 615 620

Val Ala Asn Val Thr Pro Ser Ala Ala Gly Gly Met Gly Gly Met Met  
 625 630 635 640

Asn Gly Gly Met Ala Ala Pro Gln Ser Pro Gly Met Asn Gly Gly Arg  
 645 650 655

Leu Gly Thr Asn Pro Leu Phe Asn Ala Ala Pro Ser Pro Leu Ser Ser  
 660 665 670

Gln Leu Gly Ala Glu Ala Gly Met Gly Ser Met Gly Gly Met Gly Gly  
 675 680 685

Met Ser Gly Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly Ala  
 690 695 700

Gly Ala Ala Thr Thr Gln Ala Ala Gly Gly Asn Ala Glu Ala Glu Met  
 705 710 715 720

Leu Gln Asn Leu Met Asn Glu Ile Asn Arg Leu Lys Arg Glu Leu Gly  
 725 730 735

Glu

<210> 3

<211> 259

<212> PRT

<213> Halobacterium salinarum

<220>

<223> Amino acid sequence of bacteriorhodopsin from  
 Halobacterium salinarum

<400> 3

Met Leu Pro Thr Ala Val Glu Gly Val Ser Gln Ala Gln Ile Thr Gly  
 1 5 10 15

Arg Pro Glu Trp Ile Trp Leu Ala Leu Gly Thr Ala Leu Met Gly Leu  
 20 25 30

Gly Thr Leu Tyr Phe Leu Val Lys Gly Met Gly Val Ser Asp Pro Asp  
 35 40 45

Ala Lys Lys Phe Tyr Ala Ile Thr Thr Leu Val Pro Ala Ile Ala Phe  
 50 55 60

Thr Met Tyr Leu Ser Met Leu Leu Gly Tyr Gly Leu Thr Met Val Pro  
 65 70 75 80

Phe Gly Gly Glu Gln Asn Pro Ile Tyr Trp Ala Arg Tyr Ala Asp Trp

85	90	95
Leu Phe Thr Thr Pro Leu Leu Leu Leu Asp Leu Ala Leu Leu Val Asp		
100	105	110
Ala Asp Gln Gly Thr Ile Leu Ala Leu Val Gly Ala Asp Gly Ile Met		
115	120	125
Ile Gly Thr Gly Leu Val Gly Ala Leu Thr Lys Val Tyr Ser Tyr Arg		
130	135	140
Phe Val Trp Trp Ala Ile Ser Thr Ala Ala Met Leu Tyr Ile Leu Tyr		
145	150	155
160		
Val Leu Phe Phe Gly Phe Thr Ser Lys Ala Glu Ser Met Arg Pro Glu		
165	170	175
Val Ala Ser Thr Phe Lys Val Leu Arg Asn Val Thr Val Val Leu Trp		
180	185	190
Ser Ala Tyr Pro Val Val Trp Leu Ile Gly Ser Glu Gly Ala Gly Ile		
195	200	205
Val Pro Leu Asn Ile Glu Thr Leu Leu Phe Met Val Leu Asp Val Ser		
210	215	220
Ala Lys Val Gly Phe Gly Leu Ile Leu Leu Arg Ser Arg Ala Ile Phe		
225	230	235
240		
Gly Glu Ala Glu Ala Pro Glu Pro Ser Ala Gly Asp Gly Ala Ala Ala		
245	250	255
Thr Ser Asp		

<210> 4

<211> 315

<212> PRT

<213> Chlamydomonas reinhardtii

<220>

<223> Amino acid sequence of the CHOP2-315/H134R mutant

<400> 4

Met Asp Tyr Gly Gly Ala Leu Ser Ala Val Gly Arg Glu Leu Leu Phe			
1	5	10	15

Val Thr Asn Pro Val Val Asn Gly Ser Val Leu Val Pro Glu Asp		
20	25	30

Gln Cys Tyr Cys Ala Gly Trp Ile Glu Ser Arg Gly Thr Asn Gly Ala		
35	40	45

Gln Thr Ala Ser Asn Val Leu Gln Trp Leu Ala Ala Gly Phe Ser Ile  
 50 55 60

Leu Leu Leu Met Phe Tyr Ala Tyr Gln Thr Trp Lys Ser Thr Cys Gly  
 65 70 75 80

Trp Glu Glu Ile Tyr Val Cys Ala Ile Glu Met Val Lys Val Ile Leu  
 85 90 95

Glu Phe Phe Phe Glu Phe Lys Asn Pro Ser Met Leu Tyr Leu Ala Thr  
 100 105 110

Gly His Arg Val Gln Trp Leu Arg Tyr Ala Glu Trp Leu Leu Thr Cys  
 115 120 125

Pro Val Ile Leu Ile Arg Leu Ser Asn Leu Thr Gly Leu Ser Asn Asp  
 130 135 140

Tyr Ser Arg Arg Thr Met Gly Leu Leu Val Ser Asp Ile Gly Thr Ile  
 145 150 155 160

Val Trp Gly Ala Thr Ser Ala Met Ala Thr Gly Tyr Val Lys Val Ile  
 165 170 175

Phe Phe Cys Leu Gly Leu Cys Tyr Gly Ala Asn Thr Phe Phe His Ala  
 180 185 190

Ala Lys Ala Tyr Ile Glu Gly Tyr His Thr Val Pro Lys Gly Arg Cys  
 195 200 205

Arg Gln Val Val Thr Gly Met Ala Trp Leu Phe Phe Val Ser Trp Gly  
 210 215 220

Met Phe Pro Ile Leu Phe Ile Leu Gly Pro Glu Gly Phe Gly Val Leu  
 225 230 235 240

Ser Val Tyr Gly Ser Thr Val Gly His Thr Ile Ile Asp Leu Met Ser  
 245 250 255

Lys Asn Cys Trp Gly Leu Leu Gly His Tyr Leu Arg Val Leu Ile His  
 260 265 270

Glu His Ile Leu Ile His Gly Asp Ile Arg Lys Thr Thr Lys Leu Asn  
275                    280                    285

Ile Gly Gly Thr Glu Ile Glu Val Glu Thr Leu Val Glu Asp Glu Ala  
290                    295                    300

Glu Ala Gly Ala Val Asn Lys Gly Thr Gly Lys  
305                    310                    315